

FIGURE 1A

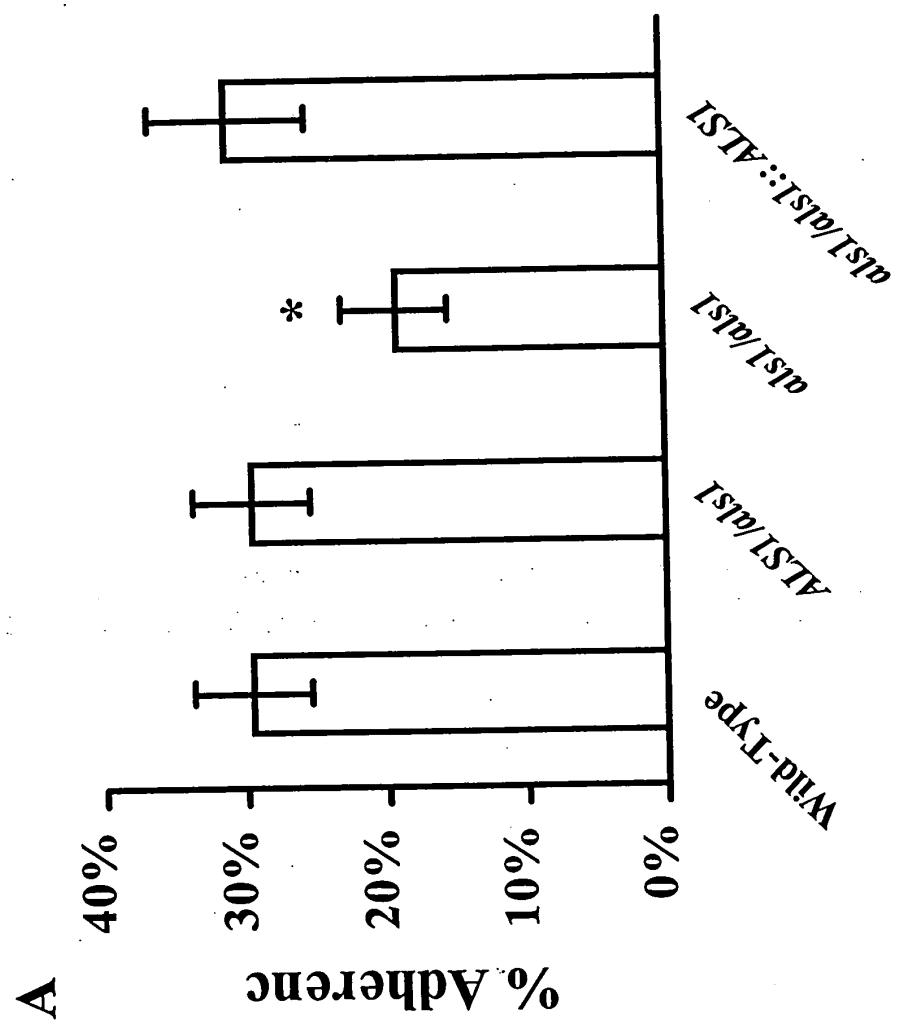
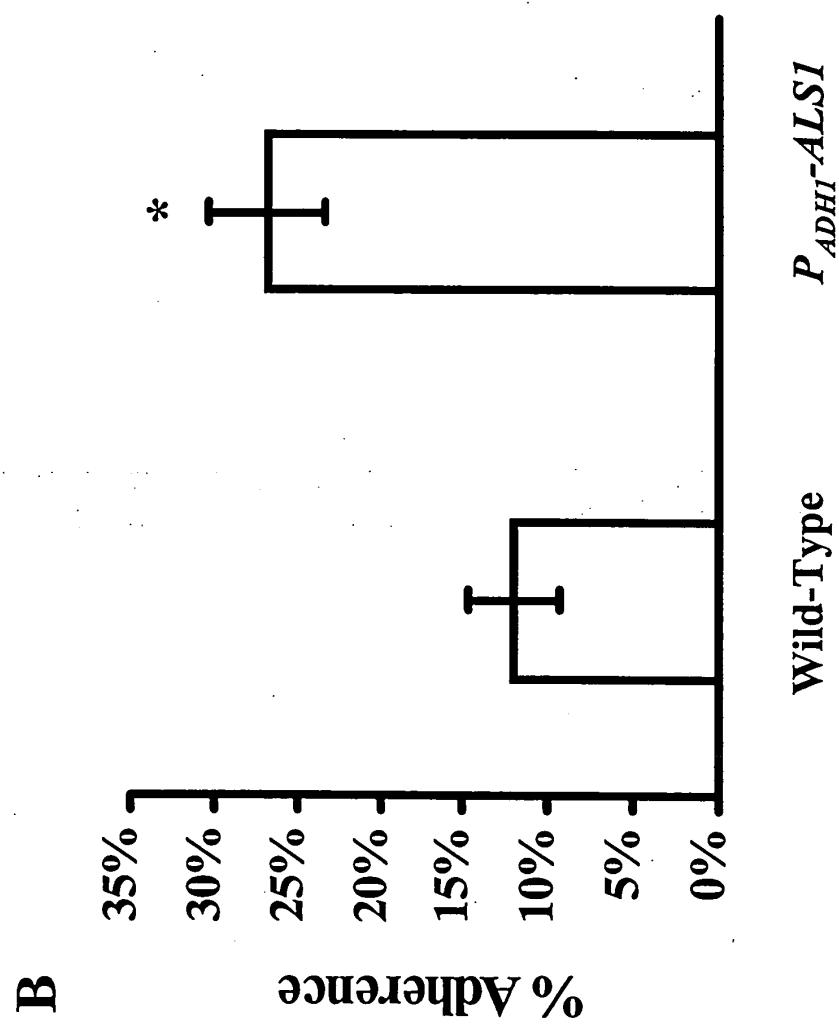
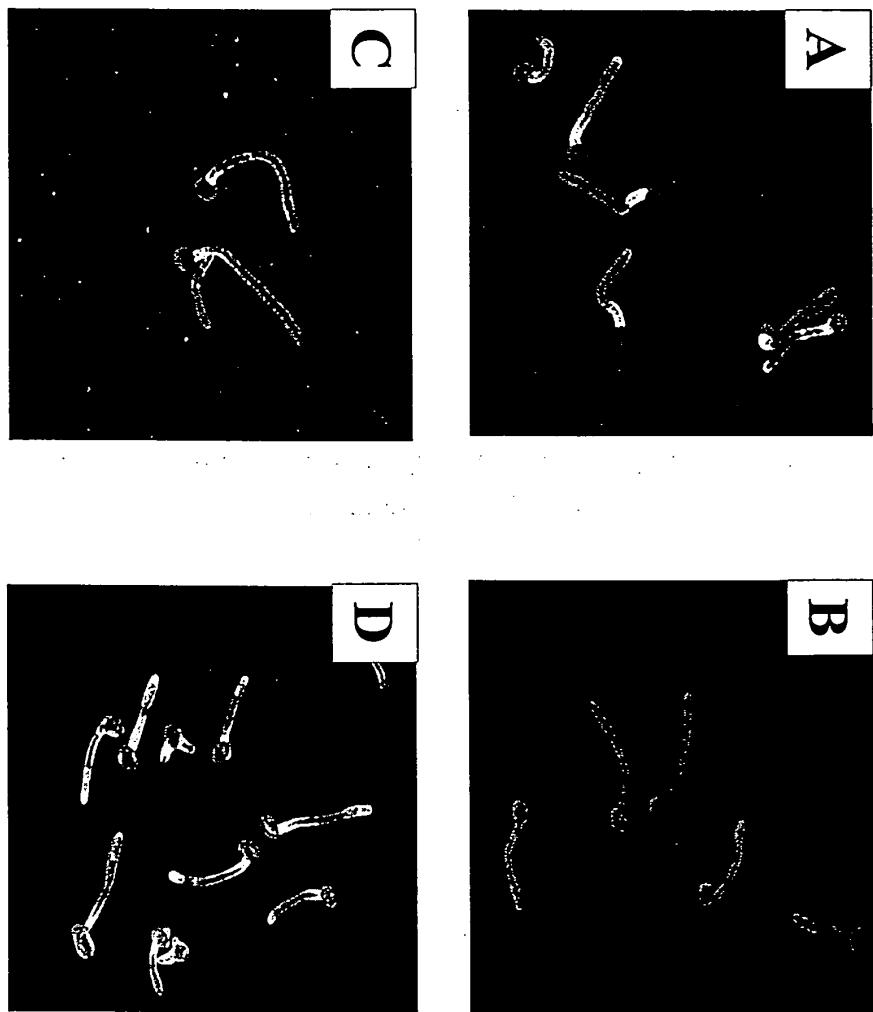


FIGURE 1B





FIGURES 2A, 2B, 2C, 2D

FIGURE 3A



Wild-Type

A



als1/als1

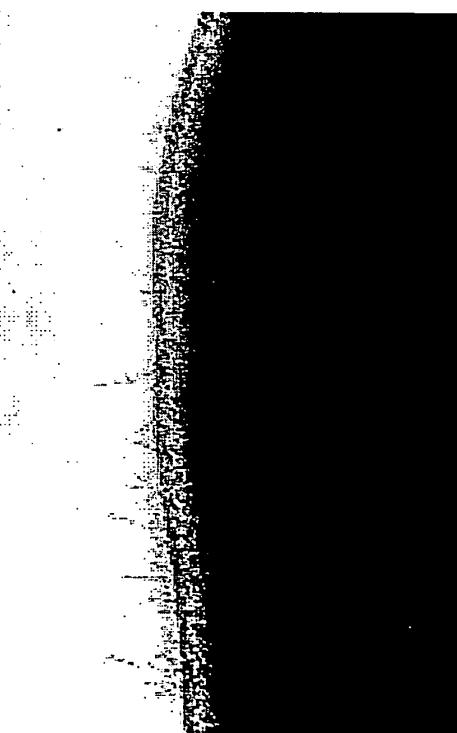
als1/als1::ALS1

FIGURE 3B

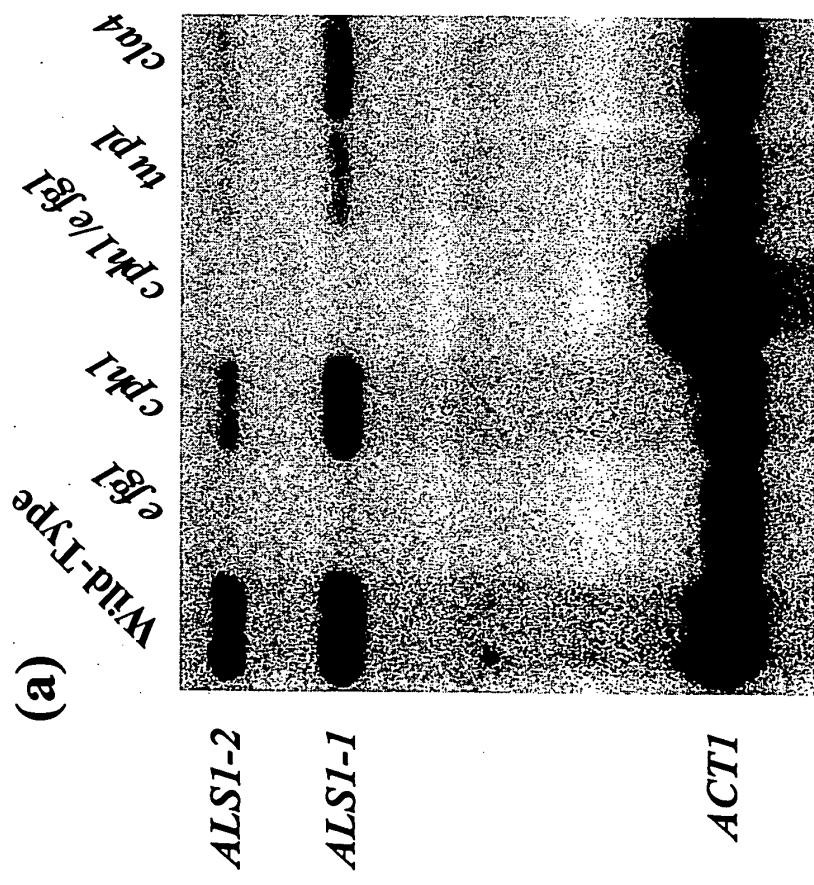
P_{ADH1-ALS1}

Wild-Type

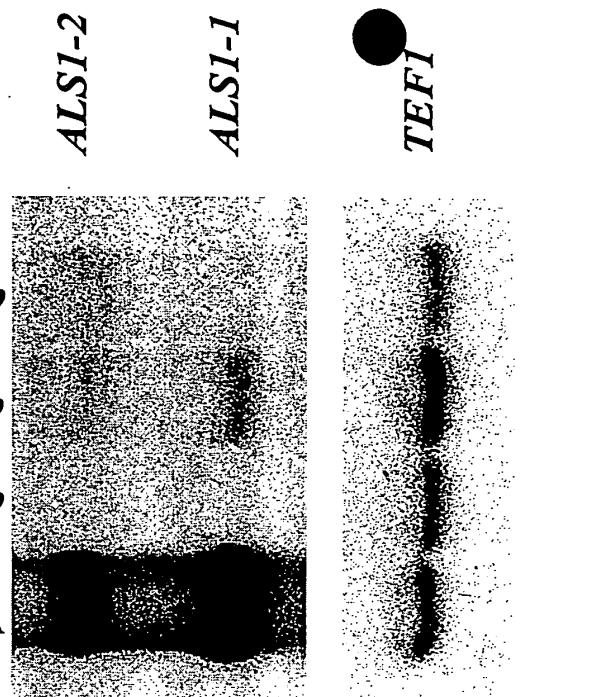
B



A

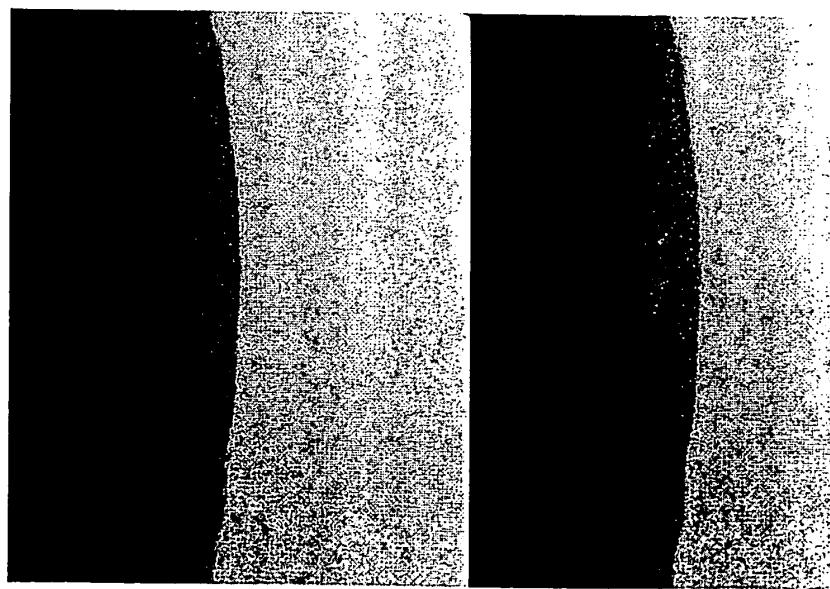


(b)



B

efg1/efg1



efg1/efg1, P_{ADH1} ALS1

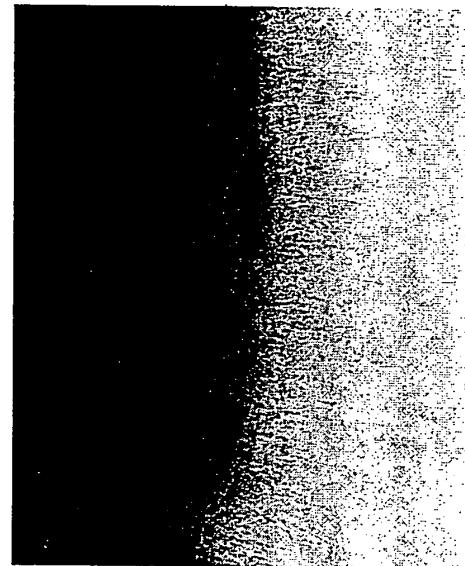
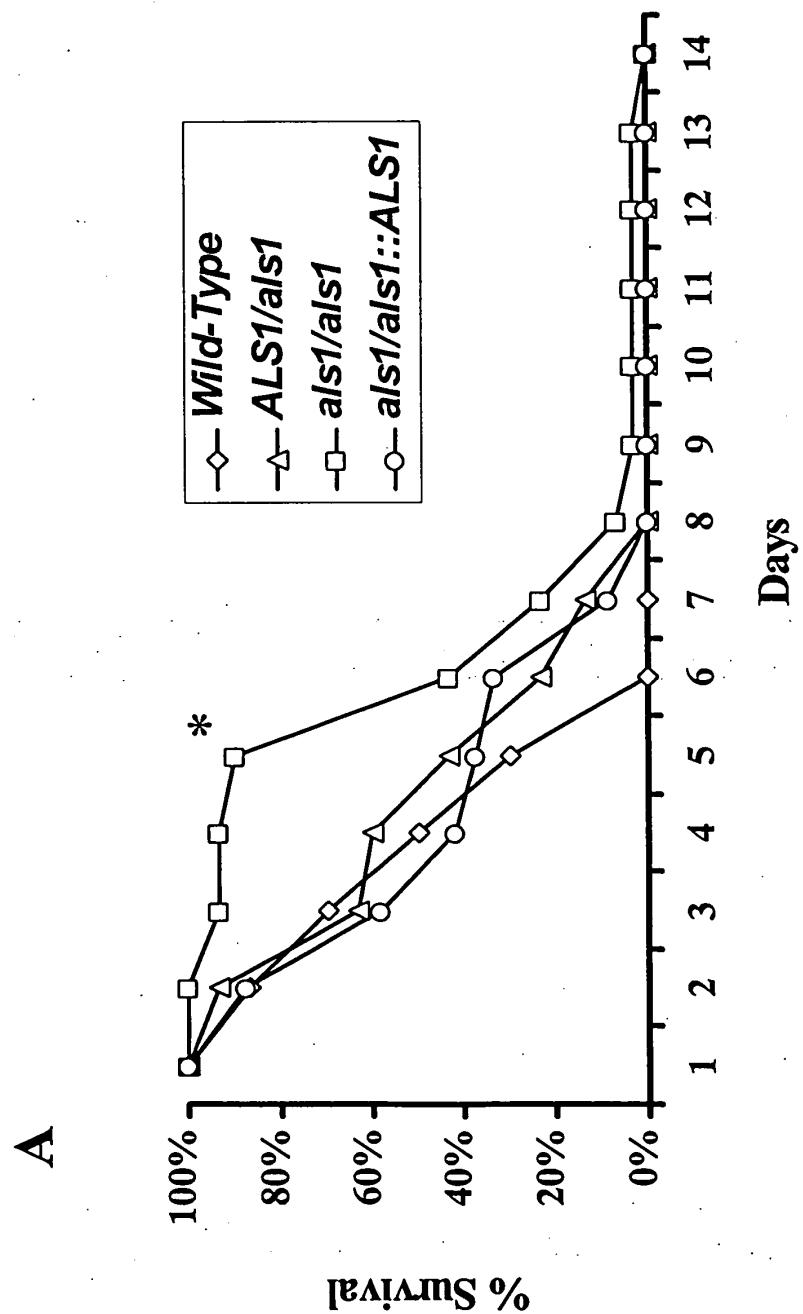


FIGURE 4B

FIGURE 5A

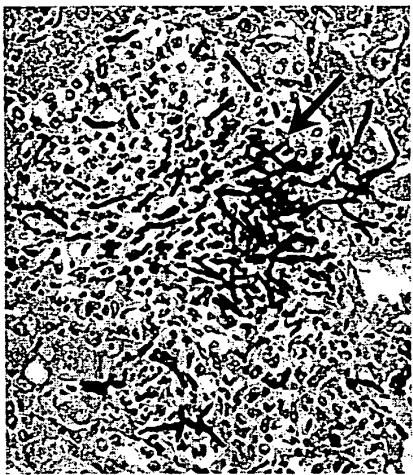


B

a Wild-Type



als1/als1::ALS1



b Wild-Type



als1/als1

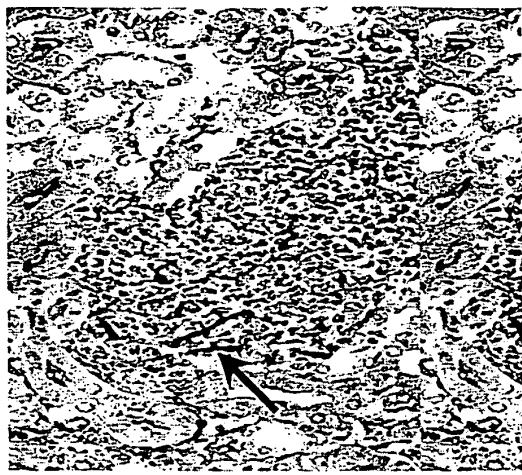
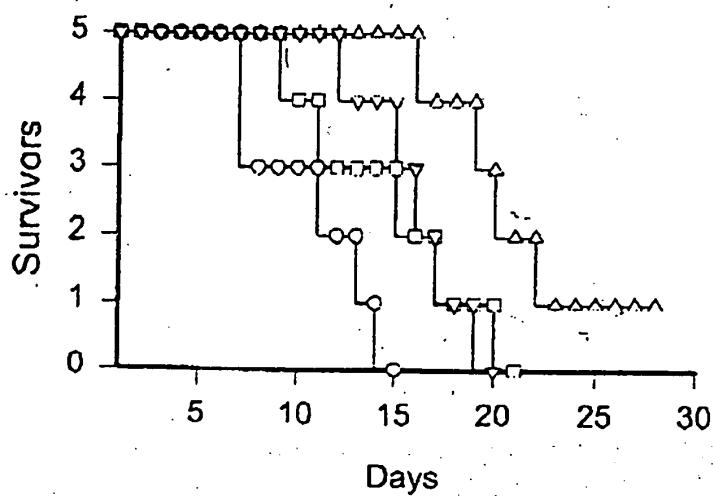


FIGURE 5B

Prophylactic effect of antiALS antibody against disseminated candidiasis



MST (days)

—○— DPBS	11.4 ± 3.3
—□— NRS (PB) ¹	15.4 ± 4.4
—△— S ² -antiALS	22.0 ± 4.5
—▽— I ³ -antiALS	16.8 ± 2.6

FIGURE 6

500
450
400
350
300
250
200
150

1 ATGCTTCAACAATTTACATTGTTATTCCATATTTGTCATTGCAAGTGCAAAGACAATC
1 M L Q Q F T L L F L Y L S I A S A K T I
61 ACTGGTGTGTTGATAGTTAATTCACTGGTCCAATGCTGCTAATTATGCTTTC
21 T G V F D S F N S L T W S N A A N Y A F
121 AAAGGGCCAGGATACCCAACTTGGAAATGCTGTTGGGTTGGCCTAGATGGTACCAAGT
41 K G P G Y P T W N A V L G W S L D G T S
181 GCCAATCCAGGGATACATTCACATTGAATATGCCATGTGTTAAATATACTACTTCA
61 A N P G D T F T L N M P C V F K Y T T S
241 CAAACATCTGTTGATTAACCTGCCATGGTAAATATGCTACTGTCAATTGTTATTCT
81 Q T S V D L T A D G V K Y A T C Q F Y S
301 GGTGAAGAATTACAACCTTTCTACATTAACATGTACTGTGAACGACGCTTGAAATCA
101 G E E F T T F S T L T C T V N D A L K S
361 TCCATTAAGGCATTGGTACAGTTACCAATTGCATTCAATGTTGGTGGAACAGGT
121 S I K A F G T V T L P I A F N V G G T G
421 TCATCAACTGATTGGAAGATTCTAAATGTTTACTGCTGGTACCAATACAGTCACATT
141 S S T D L E D S K C F T A G T N T V T F
481 AATGATGGTGATAAAAGATATCTCAATTGATGTTGAGTTGAAAGTCACCGTTGATCCA
161 N D G D K D I S I D V E F E K S T V D P
541 AGTGCATATTGTTGCTACAGTTACCAATTGCAAGTCTCAATAAGGTACAACTCTTTT
181 S A Y L Y A S R V M P S L N K V T T L F
601 GTGGCACCAATGTGAAATGGTTACACATCTGGTACAATGGGTTCTCCAGTAGTAAC
201 V A P Q C E N G Y T S G T M G F S S S N
661 GGTGACGTTGCTATTGATTGCTCAAATATTCAATTGGTATCACAAAAGGATTAATGAT
221 G D V A I D C S N I H I G I T K G L N D
721 TGGAATTATCCGGTTCATCTGAATCATTTAGTACACTAAAACCTTGTCACATCTAATGGA
241 W N Y P V S S E S F S Y T K T C T S N G
781 ATTCAAGATTAATATCAAAATGTACCTGCTGGTTATCGTCCATTATTGATGCTTATATT
261 I Q I K Y Q N V P A G Y R P F I D A Y I
841 TCTGCTACAGATGTTACCAATATACTTACATACCAATGATTATACTTGTGCTGGC
281 S A T D V N Q Y T L A Y T N D Y T C A G
901 AGTCGTCTGCAAAGTAAACCTTCACTTAACATGGACTGGATACAAGAATAGTGATGCC
301 S R L Q S K P F T L R W T G Y K N S D A
961 GGATCTAACGGTATTGTCATTGTTGCTACAACACTAGAACAGTTACAGACAGTACCACTGCT
321 G S N G I V I V A T T R T V T D S T T A
1021 GTCACTACTTACCAATTCAATCCAAGTGTGATAAAACCAAAACAATCGAAATTTGCAA

FIGURE 7

341 V T T L P F N P S V D K T K T I E I L Q
 1081 CCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCCTATCTGACT
 361 P I P T T T I T T S Y V G V T T S Y L T
 1141 AAGACTGCACCAATTGGTGAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACC
 381 K T A P I G E T A T V I V D V P Y H T T
 1201 ACAACTGTTACCACTGAATGGACAGGAACAATCACTACCACCAACTCGTACCAATCCA
 401 T T V T S E W T G T I T T T T R T N P
 1261 ACTGATTCAATTGACACAGTGGTGTACAAGTTCCACTGCCAAATCCAACGTGTTAGTACT
 421 T D S I D T V V V Q V P L P N P T V S T
 1321 ACTGAATATTGGTCTCAGTCCTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGT
 441 T E Y W S Q S F A T T T T V T A P P G G
 1381 ACCGATACTGTGATTATCAGAGAGCCACCAACCATACTGTCACTACTACTGAATATTGG
 461 T D T V I I R E P P N H T V T T T E Y W
 1441 TCACAATCCTTGCTACTACTACTGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA
 481 S Q S F A T T T V T A P P G G T D S V
 1501 ATTATCAGAGAACCAACCAAATCCAACGTGCACTACAACCGAGTATTGGTCTCAATCCTT
 501 I I R E P P N P T V T T T E Y W S Q S F
 1561 GCTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAA
 521 A T T T T V T A P P G G T D S V I I R E
 1621 CCTCCAAACCCAACTGTCACCAACCACTGAATATTGGTCCCAATCTTACGCAACCAACT
 541 P P N P T V T T E Y W S Q S Y A T T T
 1681 ACTGTGACTGCTCCTCCAGGAGGCAGTGAACGTAAATTATCAGAGAACCAACCAAC
 561 T V T A P P G G T D S V I I R E P P N H
 1741 ACTGTCACTACTGAATACTGGTCACAAATCATATGCCACCAACTACACTGTAACGTCA
 581 T V T T E Y W S Q S Y A T T T T V T A
 1801 CCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCACCAACACTGTCACTACT
 601 P P G G T D T V I I R E P P N H T V T T
 1861 ACTGAGTATTGGTCTCAATCGTTGCTACTACCAACACTGTAACGTCCACCAAGTGGC
 621 T E Y W S Q S F A T T T V T G P P S G
 1921 ACTGATACTGTTATCATTAGGAAACCAACCAACCAACTGTCACCAACTACTGAATACTGG
 641 T D T V I I R E P P N P T V T T T E Y W
 1981 TCTCAATCATATGCAACCACTACTACCAATTACCGCTCCACCTGGTGAACACTGATAACCGTT
 661 S Q S Y A T T T I T A P P G E T D T V
 2041 CTTATCAGAGAGCCACCAACCAACTGTCACCAACTACTGAATACTGGTCTCAATCATAT
 681 L I R E P P N H T V T T T E Y W S Q S Y
 2101 GCTACAACCAACCACTGTTACTGTCACCAACCTGGTGAACCGATAACCGTTCTTACAGAGAG
 701 A T T T T V T A P P G E T D T V L I R E
 2161 CCACCAAACCAACTGTCACCAACTACTGAATACTGGTCTCAATCATATGCTACAAACCAAC

FIGURE 7

721 P P N H T V T T E Y W S Q S Y A T T T
 2221 ACTGTTACTGCACCAACCAGGGTACCGATACTGTTATCATTAGAGAGCCACCAAATCCA
 741 T V T A P P G G T D T V I I R E P P N P
 2281 ACAGTTACTACTGAATATTGGTCACAATCATTGCCACAACCACAGTTACTGCT
 761 T V T T T E Y W S Q S F A T T T T V T A
 2341 CCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGTCAAGTTCAAAGATTCT
 781 P P G G T D T V I I Y E S M S S S K I S
 2401 ACATCCTCCAATGATATAACCAGTATCATTCCATCTTCCGTCCTCATTATGTCAAC
 801 T S S N D I T S I I P S F S R P H Y V N
 2461 AGCACAACCTCCGATTGTCAACATTGAAATCTTCATCCATGAATACTCCTACTTCTATC
 821 S T T S D L S T F E S S S M N T P T S I
 2521 AGTAGTGATGGTATGTTGTTCTACAACATTGGTTACTGAATCAGAAACAACATACA
 841 S S D G M L L S S T T L V T E S E T T T
 2581 GAACTGATTGCACTGATGGTAAAGAGTGTCTAGATTGTCCAGTTCTCTGGTATTGTC
 861 E L I C S D G K E C S R L S S S S G I V
 2641 ACAAACTCCAGATAGCAATGAATCCTCAATCGTAACTAGTACTGTTCCACTGCAAGTACA
 881 T N P D S N E S S I V T S T V P T A S T
 2701 ATGTCGATTCACTTCTTCAACTGATGGTATTAGTGTACATCTCTGATAATGTTCA
 901 M S D S L S S T D G I S A T S S D N V S
 2761 AAATCAGGAGTATCAGTTACAACCGAAACTCTGTTACAACATTCAAACACTCCAAAC
 921 K S G V S V T T E T S V T T I Q T T P N
 2821 CCATTATCATCTTCAGTGACATCATTGACTCAGTTGTCCTCAATTCCAAGTGTTCAGAA
 941 P L S S S V T S L T Q L S S I P S V S E
 2881 AGTGAAGTAAAGTTACATTACAAGCAATGGAGACAACCAAGTGGTACTCATGATTCA
 961 S E S K V T F T S N G D N Q S G T H D S
 2941 CAATCTACTTCACTGAAATTGAAATTGTAACAACCAACAGTTCTACTAAAGTTTACCACT
 981 Q S T S T E I E I V T T S S T K V L P P
 3001 GTCGTTCTTCTAATACTGATTTGACTAGTGAACCAACAAATACCAAGAGAACACCAACT
 1001 V V S S N T D L T S E P T N T R E Q P T
 3061 ACATTATCAACTACTCAAACCTCCATCACTGAAGATATCACCACATCTCAACCTACAGGT
 1021 T L S T T S N S I T E D I T T S Q P T G
 3121 GATAATGGAGACAATACTTCATCAACCAATCCAGTTCAACTGTGGCAACAAGTACTTTA
 1041 D N G D N T S S T N P V P T V A T S T L
 3181 GCATCTGCAAGTGAAGAAGACAACAAAGCGGTTCTCATGAATCAGCATCCACAAGTTG
 1061 A S A S E E D N K S G S H E S A S T S L
 3241 AAACCAAGTATGGGTAAAATTCTGGATTAACACTTCTACTGAAATTGAAGCTACAACA
 1081 K P S M G E N S G L T T S T E I E A T T
 3301 ACCAGTCCTACAGAAGCTCCATCACCTGCTGTTCTGGTACTGATGTAACACTGAA

FIGURE 7

1101 T S P T E A P S P A V S S G T D V T T E
3361 CCAACTGATACTAGAGAACAAACCTACTACATTATCAACTACTTCAAAACAAACAGTGAA
1121 P T D T R E Q P T T L S T T S K T N S E
3421 CTGGTTGCTACTACACAAGCTACTAATGAAAATGGTGGTAAATCTCCATCAACTGATTAA
1141 L V A T T Q A T N E N G G K S P S T D L
3481 ACATCAAGCTTGACAACAGGCACCTCAGCATCTACAAGTGCTAATAGCGAACTTGTACT
1161 T S S L T T G T S A S T S A N S E L V T
3541 AGTGGATCTGTTACTGGTGGAGCTGTTGCCAGTGCTTCATGATCAATCACATTCTACT
1181 S G S V T G G A V A S A S N D Q S H S T
3601 TCTGTTACCAACAGCAACAGCATTGTATCTAATACCCCACAAACTACATTGAGTCAACAA
1201 S V T N S N S I V S N T P Q T T L S Q Q
3661 GTTACCTCATCCTCACCTCAACCAACACATTGCTTCTACATACGATGGCTCTGGT
1221 V T S S S P S T N T F I A S T Y D G S G
3721 TCTATTATCCAACATTCTACTTGGTTGACGGTTGATCACATTATTGTCCTTGTTCATT
1241 S I I Q H S T W L Y G L I T L L S L F I
3781 TAGTGA
1261 * *

FIGURE 7